Online-Only Abstract

Single nucleotide polymorphism-based molecular typing of *M. leprae* from multicase families of leprosy patients and their surroundings to understand the transmission of leprosy

R. P. Turankar[1], M. Lavania[1], V. S. Chaitanya[1], U. Sengupta[1], J. Darlong[2], F. Darlong[2], K. S. R. Siva Sai[3] and R. S. Jadhav[1,4]

1) *Stanley Browne Laboratory, The Leprosy Mission, Community Hospital Nand Nagari, Delhi,* 2) *Out Patient Department, Purulia Hospital, The Leprosy Mission, Purulia* 3) *Department of Biotechnology, Sreenidhi Institute of Science and Technology, Hyderabad and* 4) *Department of Microbiology, Government Institute of Science, Mumbai, India*

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Abstract

The exact mode of transmission of leprosy is not clearly understood; however, many studies have demonstrated active transmission of leprosy around a source case. Families of five active leprosy cases and their household contacts were chosen from a high endemic area in Purulia. Fifty-two soil samples were also collected from different areas of their houses. DNA was extracted from slit-skin smears (SSS) and soil samples and the *Mycobacterium leprae*-specific RLEP (129 bp) region was amplified using PCR. Molecular typing of *M. leprae* was performed for all RLEP PCR-positive samples by single nucleotide polymorphism (SNP) typing and confirmation by DNA sequencing. SSS of these five patients and six out of the total 28 contacts were PCR positive for RLEP whereas 17 soil samples out of 52 showed the presence of *M. leprae* DNA. SNP typing of *M. leprae* from all RLEP PCR-positive subjects (patients and smear-positive contacts) and 10 soil samples showed the SNP type 1 genotype. *M. leprae* DNA from the five leprosy patients and the six contacts was further subtyped and the D subtype was noted in all patients and contacts, except for one contact where the C subtype was identified. Typing followed by subtyping of *M. leprae* clearly revealed that either the contacts were infected by the patients or both patients and contacts had the same source of infection. It also revealed that the type of *M. leprae* in the soil in the inhabited areas where patients resided was also of the same type as that found in patients.